Workshop Scientific Report (ESF)

Workshop: Perspectives and challenges of simulations of bio-materials interfaces

Organizers: Prof. Dr. Thomas Frauenheim, University of Bremen, Germany
Prof. Dr. Lucio Colombi Ciacchi, University of Bremen, Germany
Prof. Dr. Viola Vogel, ETH-Zuerich, Switzerland

Location: University of Bremen, Germany,
10.-14. October 2011

I. Summary

The workshop “and challenges of simulations of bio-materials interfaces” was held at the University of Bremen, Germany from October 10th to October 14th 2011. In total, 65 participants from Bulgaria, Germany, USA, UK, Canada, Denmark, Japan, Poland, Sweden, Italy, Iran, France, China and Switzerland attended the workshop.

The programme consisted of 29 invited lectures, one poster session and different social events allowing for scientific discussions and exchange. The lectures were scheduled to last 40 min, including 10 min discussion time. In addition to this extended time for discussion, the chairpersons were instructed to introduce the subject of the session and to actively participate in the discussion. This “Gordon-conference-style” was essential to guarantee a vivid discussion. The organizers ensured that well-established scientists acted as invited speakers and chairpersons.

Concerning the poster session, we accepted only 22 posters to allow for an intense exchange of ideas at each single poster. Here, we encouraged in particular the young scientists to ask questions. The participation of young researchers were supported by partly covering local accommodation costs.

Due to the compact organization and accommodation in one hotel only all participants had to stay together for the whole time of the conference, which additionally enforced the scientific discussion which was mandatory since scientists from various separated fields, i.e. advanced quantum chemistry, quantum Monte-Carlo, many-body perturbation theory, time-dependent DFT, etc. were attending the meeting to merge ideas and formulate a common goal for future method developments.

Financial support from the European Science Foundation (ESF), Psi-k Charity, the German CECAM node multiscale modelling from first principles, cecam-mm1p.de, the Deutsche Forschungsgemeinschaft (DFG) and the University Bremen is gratefully acknowledged.

II. Scientific content and discussion

The physical/chemical behavior of hybrid bio-organic/inorganic interfaces in the focus of the workshop results from a delicate interplay between the electronic or mechanical properties of the inorganic phase and the surface bonding of biological molecules, which may undergo a drastic change of their structure and thus of their functionality upon interaction with the solid. Chemical reactions at the phase boundaries and other processes involving the transfer of electrons or the exchange of ions across the interface characterize uniquely the behavior of the composite material. Since such effects are not trivial to be analyzed with high resolution experiments or predicted a priori, computer modeling offers a viable way to investigate them on the basis of fundamental physical principles, thus complementing and expanding the information obtained by means of experimental techniques.

The investigation of phenomena at hybrid biomaterials interfaces poses so far unresolved challenges to accurate, atomistic computational methods, since it involves dealing with mutually interacting phenomena spanning multiple time and length scales and requiring different levels of precision. In the biological community, deciphering the physics of complex units from motor proteins to ribosomes, from membrane channels to DNA packaging in the cell nucleus or DNA-sequencing has become possible by the advent of many new technologies to analyze and manipulate molecular systems at highest precision. Combining high-resolution structural analysis with high-performance computing enabled furthermore to simulate how the intrinsic structural movements of biological nano-scale systems combined with their optical, electrical or mechanical properties control or regulate their functions. Also aided by high-performance computing, new functional hybrid-materials were designed, some of which were inspired by biological systems. Understanding life from its molecular foundation on a qualitative level, learning from it for technical applications and elucidating how the interactions between living structures interact and the technical world may stimulate novel routes for materials design has become a very attractive field of research these days.

To accomplish this goal successfully computational research request different methods from quantum and classical atomistic simulations through coarse grained techniques and further bottom upscale to finite element methods (FEM), and this is done traditionally in quite separate research communities.

Since the subject of the workshop is so interdisciplinary, also the background and scientific communities of the lecturers and participants were quite diverse. It was therefore the aim of the workshop to familiarize the participants with different subjects, to encourage interdisciplinary interactions, and to share experience of different research fields with one another. In this way, we managed to foster the exchange of ideas and methods, to highlight the most recent advances in experiments and computational method developments and applications, and hopefully stimulated new and fruitful collaborations and future projects across subject boundaries.

III. Assessment of the results and impact on future direction of the field

It became apparent from the presentations and the corresponding discussions that the modelling in each component of bio-materials interfaces is indeed very challenging. In some areas of the research field the methods and approaches have still not matured, so that intrinsic technical and conceptual problems persist.

In the workshop the following key objectives have been achieve:

The main advantages and disadvantages of currently available modeling techniques for the specific case of simulations of biological/inorganic interfaces have been discussed and specified. The techniques considered comprise (but not are limited to): (i) QM: essentially DFT-based techniques for ground states configurational sampling, including Order-N techniques; (ii) MM: atomistic force fields and many-body potentials; (iii) QM/MM: hybrid quantum/classical with static QM zones; (iv) D-QM/MM: hybrid quantum classical with dynamically moving and evolving QM zones; (v) CG: coarse-grained; (vi) HCG hybrid coarse-grained coupling different levels of precision.

The workshop impressively demonstrated the already existing intense collaboration between experiment and theory being the basis for improving our understanding of fundamental interactions and the functional interplay at bio-materials interfaces. To foster this process even further invited overview talks by highly recognized experimentalists have been presented.

In the workshop future directions for method developments and improvements of existing techniques to address physical and chemical phenomena at bio-organic/inorganic interfaces have been discussed. This has set the basis for scientific collaborations between the participants in order to foster methodological advances with respect to the state of the art.

October 19th 2011

The Organizers

CECAM – Workshop

Perspectives and challenges of simulations at bio-materials interfaces

---

October 10th -14th 2011

Bremen Center for Computational Materials Science
University of Bremen

Conference Organisers

Prof. Dr. Lucio Colombi Ciacchi

University of Bremen
Bremen Center for Computational Materials Science (BCCMS)
Am Fallturm 1
28359 Bremen, Germany

Tel.: +49(0)421/218-64570
Fax: +49(0)421/218-64599
E-mail:colombi [at] hmi.uni-bremen.de
Web: http://www.hmi.uni-bremen.de/Colombi_Ciacchi/colombi_home.html

Prof. Dr. Thomas Frauenheim

University of Bremen
Bremen Center for Computational Materials Science (BCCMS)
Am Fallturm 1
28359 Bremen, Germany

Tel.: +49(0)421/218-62340
Fax: +49(0)421/218-62770
E-mail: frauenheim [at] bccms.uni-bremen.de
Web: http://www.bccms.uni-bremen.de/en/people/home/th_frauenheim

Prof. Dr. Viola Vogel

Swiss Federal Institute of Technology
Wolfgang-Pauli-Str. 10
8093 Zurich, Switzerland

Tel.: +41(0) 44 632 08 87
Fax: +41(0) 44 632 10 73
E-mail:viola.vogel [at] mat.ethz.ch
Web: http://www.nanomat.mat.ethz.ch/people/head/vogelv

Program of the International CECAM-Workshop

"Perspectives and challenges of simulations at bio-materials interfaces"

Bremen Center for Computational Material Science - BCCMS

University of Bremen, October 10 - 14, 2011

Conference site: "House of Science" Downtown - BCCMS - University Campus

Monday, October 10th 2011 (Best Western Hotel Schaper Siedenburg)

18:00 – 22:00 Registration

Tuesday, October 11th 2011 (House of Science – Downtown)

08:00-08:50 Registration

08:50-09:00 Opening and welcome, Lucio Colombi Ciacchi / Thomas Frauenheim

Session: Surfaces I

Chair: Viola Vogel

09:00-09:40 Klaus Schulten, University of Illinois at Urbana-Champaign, (USA)
Computer modeling in biotechnology, a partner in development

09:40-10:20 Elisa Molinari University of Modena (Italy)
Protein specific adhesion on the gold surface in water by first principle simulations

10:20-10:50 Coffee Break

10:50-11:30 Kurosch Rezwan, University of Bremen (Germany)
Antibacterial surface functionalisation

11:30-12:10 Alessandro de Vita, Kings College London (UK)
Supramolecular self-assembly at surfaces: from direct linkage to long range interactions

12:10-14:00 Lunch Break

Program of the International CECAM-Workshop

"Perspectives and challenges of simulations at bio-materials interfaces"

Bremen Center for Computational Material Science - BCCMS

University of Bremen, October 10 - 14, 2011

Conference site: "House of Science" Downtown - BCCMS - University Campus

Tuesday, October 11th 2011 (House of Science – Downtown)

Session: Surfaces II

Chair: Lucio Colombi Ciacchi

14:00-14:40 Lutz Maedler, University of Bremen (Germany)
Controlled solubility of nanoparticles in physicological environment

14:40-15:20 Tiffany Walsh, The University of Warwick (UK)
Atomistic simulations of the aqueous peptide-inorganic interface

15:20-15:50 Coffee Break

15:50-16:30 Stefano Corni, University of Modena (Italy)
Protein-gold interfaces in water: insights from atomistic simulations

16:30-17:10 Markus Buehler, Massachusetts Institute of Technology, Cambridge (USA)
Deformation and failure of protein materials in physiologically extreme conditions and disease

19:00-21:30 Welcome Reception (Bremen Town Hall)

Program of the International CECAM-Workshop

"Perspectives and challenges of simulations at bio-materials interfaces"

Bremen Center for Computational Material Science - BCCMS

University of Bremen, October 10 - 14, 2011

Conference site: "House of Science" Downtown - BCCMS - University Campus

Wednesday, October 12th 2011 (House of Science – Downtown)

Session: Biomechanics

Chair: Frauke Graeter

08:30-09:10 Ralf Seidel, Dresden University of Technology (Germany)
Nanomechanics of DNA origami

09:10-09:50 Viola Vogel, ETH Zurich (Switzerland)
Mechanisms by which forces can switch the structure-function relationships of proteins

Session: Biomineralization

Chair: Pablo Ordejón

09:50-10:30 Helmut Coelfen, University of Konstanz (Germany)
Polymers at mineral interfaces and nonclassical crystallization

10:30-11:00 **Coffee Break**

11:00-11:40 Colin Freeman, Sheffield University (UK)
What goes on at the interface between molecules and minerals?

11:40-12:20 Barbara Aichmayer, Max-Planck-Institute of Colloids and Interfaces, Potsdam (Germany)
Biogenic and biomimetic organic-inorganic hybrid particles: intracrystalline interfaces of calcite and inclusions of organic molecules

12:20-14:20 **Lunch Break**

Program of the International CECAM-Workshop

"Perspectives and challenges of simulations at bio-materials interfaces"

Bremen Center for Computational Material Science - BCCMS

University of Bremen, October 10 - 14, 2011

Conference site: "House of Science" Downtown - BCCMS - University Campus

Wednesday, October 12th 2011 (House of Science – Downtown)

Session: Computational methods and techniques I

Chair: Thomas Frauenheim

14:20-15:00 Chris-Kriton Skylaris, University of Southampton (UK)
Biomolecular interactions from linear-scaling density functional theory calculations with thousands of atoms

15:00-15:40 Sandro Scandolo,The Abdus Salam, International Centre for theoretical Physics, Trieste (Italy)
Ab-initio parametrized potentials for oxide interfaces

15:40-16:10 Coffee Break

16:10-16:50 P. Mark Rodger, The University of Warwick (UK)
Control and form of mineral nanoparticles

16:50-17:30 Gábor Csányi, University of Cambridge (UK)
Adaptive QM/MM simulations of chemical reactions in solution

19:00-23:00 Conference Dinner (Juergenshof – Bremen)

Program of the International CECAM-Workshop

"Perspectives and challenges of simulations at bio-materials interfaces"

Bremen Center for Computational Material Science - BCCMS

University of Bremen, October 10 - 14, 2011

Conference site: "House of Science" Downtown - BCCMS - University Campus

Thursday, October 13th 2011 (BCCMS – University Campus, IFW–TAB-Building)

Session: Computational methods and techniques II

Chair: Fabrizio Cleri

08:30-09:10 Sievert-Jan Marrink, University Groningen (The Netherlands)
Hybrid simulations: combining atomistic and coarse-grained force fields using virtual sites

09:10-09:50 Christine Peter, Max-Planck-Institute for Polymer Research, Mainz (Germany)
Development of multiscale simulation models for biological hybrid materials

09:50-10:30 Nico van der Vegt, Darmstadt University of Technology (Germany)
The conditional reversible work method for systematic coarse graining of complex fluids

10:30-11:00 Coffee Break

11:00-11:40 Marcus Mueller, University of Goettingen (Germany)
Simulation of soft coarse-grained models for membranes

11:40-12:20 Luigi Delle Site, Max-Planck-Institute for Polymer Research Mainz (Germany)
Multiscale modeling and simulation of Liquids and Liquid-solid interfaces

12:20-14:20 Lunch Break

Session: Mechanical properties and folding

Chair: Gianaurelio Cuniberti

14:20-15:00 Frauke Graeter, Heidelberg Institute for Theoretical Studies (HITS) (Germany)
Mechanics of biomaterials: how proteins propagate forces

15:00-15:40 Hongbin Li, University of British Columbia, Vancouver (Canada)
Tuning the mechanical properties of proteins: from single molecule to biomaterials

15:40-16:20 Roland Netz, Technical University Munich (Germany)
Simulation approaches to friction in proteins and polymers

17:00-21:00 Poster Session & Buffet (Catering Service)

Program of the International CECAM-Workshop

"Perspectives and challenges of simulations at bio-materials interfaces"

Bremen Center for Computational Material Science - BCCMS

University of Bremen, October 10 - 14, 2011

Conference site: "House of Science" Downtown - BCCMS - University Campus

Friday, October 14th 2011 (BCCMS – University Campus, IFW–TAB-Building)

Session: Particle and charge transport

Chair*: Nico van der Vegt*

08:30-09:10	Daniele Varsano, University of Rome “La Sapienza” (Italy) *Multi - scale modeling of DNA derivatives*
09:10-09:50	Gianaurelio Cuniberti, Dresden University of Technology (Germany) *Charge migration and heat phenomena in biomolecular systems: two sides of the same medal?*
09:50-10:20	**Coffee Break**
10:20-11:00	Alexei Aksimentiev, University of Illinois at Urbana-Champaign (USA) *Modeling transport of biomolecules through synthetic nanochannels*
11:00-11:40	Marcus Elstner, University of Karlsruhe (Germany) *A coarse grained QM/MM approach for the description of hole transfer in DNA and proteins*
12:00	**Departure**

Abstracts of Lectures

Computer modeling in biotechnology, a partner in development

Klaus Schulten

University of Illinois at Urbana Champaign, Department of Physics and Beckman Institute, Urbana, US

Computational modeling can be a useful partner in biotechnology, in particular, in nanodevice engineering. Such modeling guides development through nanoscale views of biomolecules and devices not available through experimental imaging methods. We illustrate the role of computational modeling, mainly of molecular dynamics, through studies: development of silicon and PET bionanodevices (nanopores) for single molecule electrical recording, development of graphene-based nanopores for single molecule recording, development of lipoprotein nanodiscs for assays of single membrane proteins, and engineering of an optical surface-based kinase assay. The four case studies show how molecular dynamics approaches were adapted to the specific technical uses. The adapted molecular dynamics simulations provided key information on device behavior as well as use of technology in basic biomedical research. The simulations revealed development opportunities, arguing that the "computational microscope"is an indispensable nanoengineering tool.

Antibacterial surface functionalisation

Kurosch Rezwan

University of Bremen, Advanced Ceramics, Bremen, Germany

Protection from biofouling and surface erosion are two of the major challenges in fluid transport and food processing systems. Biofouling is one of the main causes of bacteria associated diseases while surface abrasion diminishes system efficiency and durability. Therefore an increasing interest is put on the development of material surfaces able to simultaneously withstand microbial adhesion and surface abrasion. Advanced ceramics provide an excellent surface hardness and can be biofunctionalised for antibacterial purposes. Strategies and results of different types of modified advanced ceramic surfaces are presented and discussed. [1, 2]

References

[1] Treccani L, Maiwald M, Zollmer V, Busse M, Grathwohl G, Rezwan K. Antibacterial and Abrasion-Resistant Alumina Micropatterns. Advanced Engineering Materials (Inside Cover Page) 2009;11:B61-B6.

[2] Kroll S, Treccani L, Rezwan K, Grathwohl G. Development and characterisation of functionalised ceramic microtubes for bacteria filtration. J Membrane Science 2010;365:447-55.

Supramolecular self-assembly at surfaces: From direct linkage to long range interactions

Alessandro De Vita

King's College London, Physics Department, London, UK;
University of Trieste, Dipartimento di Ingegneria Industriale e dell'Informazione, Trieste, Italy

Supramolecular self-assembly understood as the synthesis of functional supramolecular nanostructures needing no top-down human intervention (apart from the initial choice of ingredients and environmental parameters) is held to be one of most promising routes to nanodevice fabrication. Some inspiration can be taken from biological processes, which ubiquitously involve specific chiral enantiomers such as left-handed amino acids and right-handed nucleic acids.

The size- and time-complexity of these processes make them very hard to simulate by atomistic methods. However, supramolecular assembly and stereoselectivity effects also occur in much simpler molecular systems where they are more accessible to direct experimental (e.g., STM) observation. At present we are far from having achieved a general, predictive knowledge of how to fabricate structurally stable molecular assemblies, while understanding and controlling the assembly kinetics seems to be an even more difficult problem. Still, very significant progress has been made towards these goals in the last decade, mostly achieved by investigations involving both theoretical modeling and experiment.

In this talk I will review a few such investigations, addressing the 2D self-assembly of supramolecular structures supported by metal substrates. Early examples investigate the role of chiral symmetry in determining supramolecular assembly [1] and replication [2]. More recent work addressed more complex phenomena such as the onset of deprotonation-induced phase transitions [3], and the role of surface reconstructions [4-5]. I will focus on molecular charging upon adsorption, a process which is distinctively challenging for electronic-structure-based modelling. The process is interesting per se, since knowing the electric potential surrounding individual molecules is a prerequisite to producing single molecule contact devices [6]. Also, it drives the electronic level alignment of the molecular adlayer/substrate interface, which in turn determines the properties of metal organic contacts in organic electrical devices. Furthermore, charging phenomena yield long-range electrostatic interactions between adsorbed assembly unit molecules. These make it possible to fabricate very "unlikely" low-dimensional supramolecular structures [7]. Finally, I will discuss some evidence that partially charged adsorbed alkali atoms can be used as intermolecular linkage units with chemical properties different from those of standard bridging transition metal atoms, which provides an extra handle for supramolecular structures-tuning [8].

References

[1] M.Boehringer et al., Phys.Rev.Lett. 83, 324 (1999).
[2] J.Weckesser et al., Phys. Rev. Lett. 87, 096101 (2001).
[3] D.Payer et al., Chem. Eur. J. 13, 3900 (2007).
[4] F.Klappenberger et al., Chem. Phys. Chem. 9, 2522 (2008).
[5] R.Ohmann et al., ACS Nano Article ASAP DOI: 10.1021/nn103058e (2011).
[6] L.Vitali et al., Nature Materials 9,320 (2010).

[7] Giulia Tomba et al., ACS Nano 4, 7545 (2010).
[8] N.Abdurakhmanova, A.Floris, T.-C. Tseng, A.Comisso, S.Stepanow, A.De Vita, K.Kern, in preparation.

Controlled solubility of nanoparticles in physicological environment

Lutz Maedler

University of Bremen, Foundation Institute of Materials Science (IWT), Department of Production Engineering, 28359 Bremen, Germany

The establishment of verifiably safe nanotechnology requires the development of assessment tools to identify hazardous nanomaterial properties that could be modified to improve nanomaterial safety. In this respect, the material design through flame spray pyrolysis (FSP) and material characterization is the main focus of this talk.

The assessment of cellular injury pathways in order to collect knowledge about hazardous material properties that could lead to harm to humans and the environment is an important approach. Toxic oxidative stress is evaluated with a multiparameter cytotoxicity assay and compared for titanium dioxide (TiO2), cerium oxide (CeO2), and zinc oxide (ZnO) nanoparticles in bronchial epithelial and macrophage cell lines. In these studies the dissolution of ZnO nanoparticles and Zn2+ shedding lead to a series of sublethal and lethal toxicological responses at the cellular level that was alleviated through nanoparticle design (iron doping). Iron doping changes the particle matrix and slows the rate of particle dissolution. First ab-inito molecular simulations validate these experimental findings. To determine whether iron doping of ZnO also leads to lesser toxic effects in vivo, toxicity studies were performed in rodent and zebrafish models. With these data we could show that Fe doping in ZnO is a possible safe design strategy for preventing ZnO toxicity in animals and the environment and that multiparameter cytotoxicity assays are predictive to in vivo studies.

The data have been obtained in collaboration with the groups of Andre Nel and Jeffrey I. Zink at UCLA within the Center of Environmental Implications of Nanotechnology. The molecular simulations were performed in collaboration with the group of Thomas Heine, Jacobs University.

Atomistic simulations of the aqueous peptide-inorganic interface

Tiffany R. Walsh

University of Warwick, Department of Chemistry and Centre for Scientific Computing, Coventry, CV4 7AL, U.K.

While many different peptide sequences have been now been identified as having a strong affinity for a huge range of materials[1], the question of why a given sequence binds so well while another does not remains to be properly answered. To do so will enable significant advances in the fabrication of bio-inorganic interfaces with controllable, multi-functional properties. Use of molecular simulations is one of many complementary techniques that enables us to investigate these phenomena. In this contribution, a summary of our molecular simulation work in this area will be presented. We have identified the crucial role of intra-peptide interactions in peptide-inorganic binding for both titania and silica binders [2,3], especially in the context of alanine scan experiments in revealing the molecular-level reasons for changes in titania binding upon mutation [2], and to offer plausible reasons for a drop in binding affinity for nanotube-binding mutants [4]. We have also made advances in investigating shape recognition at peptide-inorganic interfaces, an under-explored topic at present. In particular, our work exploring diameter-selectivity of nanotube solubilisation [5] revealed the importance of inter-peptide co-operative interactions for peptide binding at non-flat interfaces such as nanoparticles. Another under-explored topic we have considered is the impact of using non-ideal surfaces in our molecular simulations [6]. More recently, we have demonstrated how binding affinity can be up- or down-modulated by varying the sequence of a peptide (keeping the content fixed); we have used this approach to identify sequence motifs that appear to foster or hinder surface binding [7]. In our latest work we have investigated the phenomenon of facet-selective binding, starting with calculations of the free energy of binding of amino-acid side-chain analogs onto three different quartz surfaces [8]. Our findings suggest it will be possible to design peptide sequences that can recognize different facets of quartz.

References

[1] C. Tamerler and M. Sarikaya, Acta Biomaterialia, 3, 289 (2007).
[2] A. A. Skelton, T. Liang, T. R. Walsh, ACS Appl. Mater. Interfac., 1, 1482 (2009).
[3] E. E. Oren, R. Notman, I. W. Kim, J. S. Evans, T. R. Walsh, R. Samudrala, C. Tamerler and M. Sarikaya, Langmuir, 26, 11003 (2010).
[4] S. M. Tomasio and T. R. Walsh, J. Phys. Chem. C, 113, 8778 (2009).
[5] S. R. Friling, R. Notman and T. R. Walsh, Nanoscale, 2, 98, (2010).
[6] T. R. Walsh and S. M. Tomasio, Mol. Biosyst, 6, 1707 (2010).
[7] S. M. Tomasio and T. R. Walsh, in preparation (2011).
[8] L. B. Wright and T. R. Walsh, in preparation (2011).

Protein-gold interfaces in water: Insights from atomistic simulations

Stefano Corni

Center S3, CNR Institute of Nanoscience, Modena, Italy

Interactions between proteins and inorganic surfaces are of paramount importance for the growth of natural materials. Moreover, protein-inorganics interfaces are principals in many technological fields, such as molecular biomimetics and biotechnologies exploiting inorganic nanoparticles. In particular, gold surfaces and nanoparticles are important for applications (e.g., contacts in nanoelectronics, gold nanoparticles for nanobiotechology). However, the protein-metal interaction is particularly puzzling because it involves contributions (weak dative bonds, image interactions) that do not have a biological counterpart.

Ab initio simulations are helpful to shed light on specific aspects of the problems, such as the nature of the local interactions between the peptide, water and the metal surface [1]. However, obtaining a complete picture of protein-surface interfaces requires methods able to deal with longer time- and length-scales than those accessible to ab initio. We have contributed developing computational approaches to study the interactions between proteins and inorganic surfaces in water at various levels [2-4], following a sequential multi-scale modeling scheme. In this talk, such scheme will be presented and insights on protein-gold interfaces from our simulations will be discussed.

References

[1] Calzolari, A.; Cicero, G.; Cavazzoni, C.; Di Felice, R.; Catellani, A.; Corni, S. J. Am. Chem. Soc. 2010, 132, 4790.

[2] Iori, F.; Di Felice, R.; Molinari, E.; Corni, S. J. Comp. Chem. 2009, 30, 1465.

[3] Kokh, D. B.; Corni, S.; Winn, P. J.; Hoefling, M.; Gottschalk, K. E.; Kay, E.; Wade, R. C. J. Chem. Th. Comp. 2010, 6, 1753 [4] Di Felice, R.; Corni, S. J. Phys. Chem. Lett. 2011, 2, 1510.

Deformation and failure of protein materials in physiologically extreme conditions and disease

Markus J. Buehler

Massachusetts Institute of Technology, Laboratory for Atomistic and Molecular Mechanics (LAMM), Department of Civil and Environmental Engineering, 77 Massachusetts Ave. Room 1-235A&B, Cambridge, MA, USA;

Biology efficiently creates hierarchical structures, where initiated at nano scales, are exhibited in macro or physiological multifunctional materials to provide a variety of functional properties that include structural support, force generation or energy conversion. This is exemplified in a broad range of biological materials such as hair, skin, bone, spider silk or cells. For instance, despite its simple building blocks spider silk is one of the strongest, most extensible and toughest biological materials known, exceeding the properties of many engineered materials including steel. This is puzzling since despite its great strength, spider silk is made of some of the weakest chemical bonds known, H-bonds. Using a bottom-up computational approach that spans all scales from nano (protein) to macro (spider web) we have discovered that the great strength, extensibility of spider silk as well as the great robustness of a spider web can be explained based on its particular structural makeup that involves several hierarchical levels. Thereby, the structural confinement of H-bonds into ultra-small beta-sheet nanocrystals with dimensions of only a few nanometers is a key aspect to overcome the intrinsic limitations of H-bonds, creating mechanically strong, tough and resilient cross-linking domains between a semi-amorphous phase composed of 31 protein helices. The emergence of hierarchical structures of protein networks, fibrils, fibers and the particular geometry of a spider web further contributes to the superior performance at the macroscale, providing seemingly limitless potential to map nanoscale mechanisms towards functional space. Our work unveiled a strikingly potent material design strategy that enables silks and other biological and synthetic materials to achieve superior tunable material properties despite their simple and structurally inferior material constituents. Exploiting this concept in engineering leads to a novel materials design paradigm, where enhanced functionality is not achieved using complex building blocks but rather through the utilization of universal repetitive constitutive elements arranged in hierarchical structures that range from the atomistic scale to macroscopic spider webs. Opportunities for de novo materials design are outlined based on utilizing the universality-diversity-paradigm discovered in biological materials, and we review the application of category theory to make quantitative links between seemingly disparate fields such as protein materials, social science and music as a bottom-up engineering design tool.

Nanomechanics of DNA origami

Ralf Seidel

Dresden University of Technology, DNA motors group, Biotechnology Center, Dresden, Germany

DNA-origami is a recently developed method to design and assemble sub-micrometer sized DNA nanostructures of arbitrary shape with atomic precision. The understanding of their mechanical behavior is crucial to develop a toolbox of these nanostructures for a broad range of applications. We study the material properties of DNA origami structures by direct mechanical single-molecule manipulation using magnetic tweezers. This is a sensitive mechanical tool that allows to apply and measure tension and torsion on single microscopic objects. It uses high-speed 3D particle tracking at kHz rates to resolve nm-sized conformational changes of a molecule attached to a magnetic particle that is subjected to force in a strong magnetic field gradient. We used this technique to determine the bending and torsional rigidities of DNA multi-helix bundles assembled by the origami method. In particular we investigated 4-helix bundles of 480nm and 6-helix bundles of 400nm length. While we find the bending rigidities of these structures to be greatly increased, the torsional rigidities are only moderately augmented. This behavior can be reproduced by numerical finite-element-modeling that approximate the DNA duplexes within these structures as cylinders with isotropic mechanical properties. We also show how origami structures can be defined and rigidly attached to surfaces, which is an important prerequisite to develop structured and three-dimensional surface modifications with the help of DNA templates.

Mechanisms by which forces can switch the strukture-funktion relationships of proteins

Viola Vogel

Swiss Federal Institute of Technology Zurich (ETH), Department of Materials, Zurich Switzerland

Since the physical and biochemical properties of extracellular matrix provide critical differentiation cues to cells, from stem cells to cancer, it is of major importance to gain insights how mechanical forces alter cell function, and vice versa how cells utilize forces to adhere, as well as to actively assemble and remodel their microenvironments. At the molecular level of mechanotransduction events, we need to learn how the stretching of proteins might alter their binding sites, as well as their biochemical display. Steered molecular dynamic simulations thereby play a central role to establish structural models of intermediates in the forced unfolding pathways of proteins. Knowledge regarding the structural intermediates nowadays guides the design of many of our experiments that are aimed at establishing insights into mechano-regulated mechanisms that are exploited by cells. Deciphering how proteins can serve as mechano-chemical signalling switches is thus not only essential to learn how cells probe and respond to their environments, but it has also far reaching implications in tissue engineering, systems biology and medicine.

Polymers at mineral interfaces and nonclassical crystallization

Helmut Coelfen

University of Konstanz, Physical Chemistry, Universitaetsstr. 10, 78457 Konstanz, Germany

Mineral interfaces are of great general importance for any mineral but especially for mesoscopically structured minerals due to the great surface to volume ratio. A high energy surface will reconstitute into lower energy surfaces even on cost of surface area in a solvent. This will be demonstrated for calcite. Also, some quantitative measurements of polymer – calcite surface interactions by force spectroscopy are discussed in terms of their relevance to quantitatively understand polymer-mineral interactions. These interactions are very important for non-classical crystallization where nanoparticles can be coded for subsequent self organization by face selective polymer adsorption. Some examples for such self organization processes are given leading to so-called Mesocrystals. Following back the interaction of a polymer with a crystal or its amorphous precursor, the role of polymers in a nucleation process is of special interest since at this point, the mineral interface is established. The influence of several polymers on nucleation and even on the prenucleation phase where no mineral interface exists yet is discussed.

What goes on at the interface between molecules and minerals?

Colin L. Freeman (1), John H Harding (1), David Quigley (2,3), P. Mark Rodger (3,4), Jim J. De Yoreo (5)

(1) University of Sheffield, Dept. of Materials Science and Engineering, Sheffield, UK;
(2) University of Warwick, Department of Physics, Coventry, UK;
(3) University of Warwick, Centre for Scientific Computing, Coventry, UK;
(4) University of Warwick, Department of Chemistry, Coventry, UK, 5LBNL;
(5) The Molecular Foundry, Lawrence Berkeley National Laboratory, Berkeley, CA, US

In considering the interface between soft and hard matter we often think of the hard matter as rigid and immobile while the soft matter is readily deformed. In contrast, in the search for molecular templates for the growth of “hard” materials, the designer often thinks of the “soft” molecular shape as regular and the hard material as adaptable to this template. The interface is, however, very complex and frequently both the hard and soft materials can exert some influence upon each other, potentially in a complementary fashion.

We present series of simulations on different systems where the importance of allowing flexibility within the system is examined. In the first case we consider the use of self-assembled monolayers (SAMs) to generate particular facets of calcite. SAMs have frequently been shown to be highly selective in producing a particular crystal surface although the reasons are still uncertain [1]. We consider the effect of giving flexibility to the “soft” SAM template and how this influences the growth control [2]. In the second scenario we examine the binding of the protein ovocleidin-17 (OC-17) to an amorphous calcium carbonate surface. This protein is thought to be involved in the crystallisation of eggshell within hens and therefore its interactions with pre-crystallised material are important to understand. We examine how the molecule binds at a much more fluid interface where the loss of organised structure breaks down the organisation of the surrounding solvent water as well.

References

[1] Y.-J. Han, J. Aizenberg, Angew. Chem. Int. Ed. 42 (2003) 3668.
[2] D. Quigley, P.M. Rodger, C.L. Freeman, J.H. Harding, D.M. Duffy, J. Chem. Phys. 131 (2009) 094703.

Biogenic and biomimetic organic-inorganic hybrid particles: Intra-crystalline interfaces of calcite and inclusion of organic molecules

Barbara Aichmayer

Massachusetts Institute of Technology, Department of Chemistry, Cambridge, MA, US

Organic occlusions play an important role in controlling the structure and properties of biogenic mineral crystals. It is known that intra-crystalline organic molecules in biogenic calcite improve the fracture behavior and anisotropically distort the calcite lattice. However, the detailed structure of the crystals and the underlying processes leading to the incorporation of the organic molecules are poorly understood. Three-dimensional small- and wide-angle X-ray scattering (SAXS/WAXS) using a synchrotron microbeam enables us to study the intra-crystalline interfaces in biogenic and biomimetic hybrid particles. Prismatic calcite crystals isolated from the shell of Pinna nobilis show a pronounced SAXS intensity arising from the electron density difference between calcite and occlusions of chitin and protein. The anisotropy of the SAXS signal, which reflects the orientation of the organic-inorganic interfaces, has a fixed orientation correlation to the calcite lattice (WAXS). A comparison of native and annealed prisms, where the contrast for the latter is enhanced due to the removal of organics, indicates a preferential orientation along the highly charged (001) lattice planes, which strongly interact with negatively charged aspartate groups of the intra-crystalline proteins. Furthermore, the SAXS measurements show that the intra-crystalline interfaces are initially rough and smoothen upon a mild annealing treatment at 250°C [1]. Similar rough and well-oriented interfaces were also found in synthetic calcite crystals grown in the presence of a polyelectrolyte (poly(sodium 4-styrenesulfonate)). Our findings on biogenic and bio-inspired calcite particles containing large organic molecules with charged groups suggest that electrostatic interactions play an important role for the formation of hybrid crystals with intra-crystalline occlusions.

References

[1] C. Gilow, E. Zolotoyabko, O. Paris, P. Fratzl and B. Aichmayer, Cryst. Growth Des. 2011, 11, 2054-2058.

Biomolecular interactions from linear-scaling density functional theory calculations with thousands of atoms

Chris-Kriton Skylaris (1), Stephen Fox (1), Chris Pittock (1), Jonathan W. Essex (1), Thomas Fox (2), Christofer Tautermann(2) and Noj Malcolm (3)

(1) University of Southampton, School of Chemistry, Highfield, Southampton SO17 1BJ, UK;
(2) Department for Lead Identification and Optimization Support, Boehringer Ingelheim Pharma GmbH & Co KG, 88397 Biberach, Germany;
(3) Accelrys, 334 Cambridge Science Park, Cambridge, CB4 0WN, UK

The ability to represent accurately interactions between biomolecular assemblies at the atomic level is a prerequisite for the computational study of a variety of important problems, including drug □alvation□on and enzyme catalysis. Often such simulations are performed by empirical classical force fields which are computationally very efficient. However, even when a sufficiently accurate parameterization for each compound studied exists, the predictive abilities of force fields can be limited as they are typically not able to describe explicitly the electronic charge transfer and polarization. These limitations can be overcome to a certain extent by hybrid quantum/classical (QM/MM) approaches [1] but new issues crop up such as the relative arbitrariness of the coupling between the quantum and the classical system or the convergence of properties with the size of the quantum region. Linear-scaling first principles quantum mechanical approaches make possible calculations with thousands of atoms, such as entire proteins [2], and can be used to validate or even completely avoid the QM/MM approximation. We examine how we can use such calculations with the ONETEP linear-scaling DFT program [3], converged to near-complete basis set accuracy, to obtain free energies of binding of ligands to proteins. Further developments such as electrostatic embedding and a new minimal parameter implicit □alvation model [4] can be used to include the effect of the environment in the simulations. These techniques can be applied also to the even more challenging simulations of biomolecules interacting with surfaces or nanostructures.

References

[1] H. Lin and D. G. Truhlar, Theor. Chem. Acc. 117, 185 (2007).
[2] D. J. Cole, C.-K. Skylaris, E. Rajendra, A. R. Venkitaraman and M. C. Payne. Europhysics Letters 91, 37004 (2010); S. Fox, H. Wallnoefer, T. Fox, C. Tautermann, and C.-K. Skylaris. J. Chem. Theor. Comput. 7, 1102 (2011).
[3] C.-K. Skylaris, P. D. Haynes, A. A. Mostofi and M. C. Payne, J. Ch.

Ab-initio parameterized potentials for oxide interfaces

Sandro Scandolo

The Abdus Salam International Centre for Theoretical Physics (ICTP), Trieste, Italy

The development of accurate force-fields parameterized on ab-initio simulations is a promising way to extend the size and time constraints of ab-initio simulations. Extensive work on polarizable models for oxides has shown that accurate potentials can be constructed that reproduce faithfully the ab-initio results on homogeneous bulk phases. I will describe recent efforts aimed at extending the applicability of these methods to the description of oxide interfaces. I will focus in particular on the interfaces between silica, titania, and liquid water.

This work has been done in collaboration with Carlos Pinilla and Nicola Seriani.

Control and form of mineral nanoparticles

Mark Rodger

University of Warwick, Centre for Scientific Computing & Chemistry, Coventry, U.K.

A crucial stage in the formation of biominerals is the initial nucleation of the mineral phase. Experiments currently indicate the formation of stable precritical clusters, that subsequently deposit as an amorphous phase and then crystallise and aggregate (in some order) into the polymorphs and forms found in the the biomaterials. In this talk we will present the results of various molecular modelling studies of polymorphs and morphologies accessible to nanoparticles across a range of different sizes, and show how the stability of these different forms can be modified by the presence of biomolecules. As a specific example of the latter we will show how Ovocleidin 17---a chicken eggshell protein---changes the thermodynamic behaviour of CaCO3 nanoparticles.

Adaptive QM/MM simulations of chemica reactions in solution

Gábor Csányi

Cambridge University, Engineering Laboratory, Cambridge, UK

Chemical reactions often occur in the presence of a solvent, in particular water for biological systems. To describe such processes a quantum mechanical description of the reaction site is needed, combined with a large number of solvent molecules that affect the reaction via their electrostatic fields and free energy effects of their long-range structure. We have developed an adaptive QM/MM scheme in which some of the solvent molecules are included in the QM region and are freely reassigned between the QM and MM descriptions as they diffuse. The main distinction from other approaches is the enlargement of the QM region by a buffer for the purpose of computing accurate forces. Test systems include pure water, a nucleophilic substitution reaction of methyl chloride and the free energy of proton dissociation from a tyrosine molecule, all using density functional theory with the BLYP exchange-correlation functional as implemented in CP2K. The buffered-force QM/MM method gives accurate results as compared with periodic fully QM reference calculations. Applications to biomolecules at solid/liquid interfaces will be discussed.

Hybrid simulations: Combining atomistic and coarse-grained force fields using virtual sites

Siewert-Jan Marrink

University of Groningen, GBB Institute, Groningen, The Netherlands

In this contribution I discuss a straightforward scheme to perform hybrid all-atom (AA) - coarse grained (CG) simulations, making use of virtual sites to couple the two levels of resolution [1]. With the help of these virtual sites interactions between molecules at different levels of resolution, i.e. between CG and atomistic molecules, are treated the same way as the pure CG– CG interactions. Within the field of biomolecules, our method appears ideally suited to study e.g. protein-ligand binding or protein-protein interactions with the site of interaction modeled in full detail and the surrounding coarse-grained. The method is still in the testing phase, but I expect to show some preliminary applications.

References

[1] A.J. Rzepiela, M. Louhivuori, C. Peter, S.J. Marrink. Hybrid simulations: Combining atomistic and coarse-grained force fields using virtual sites. Phys. Chem. Chem. Phys. 13, 10437-10448, 2011.

Development of multiscale simulation models for biological hybrid materials

Christine Peter

Max Planck Institute for Polymer Research, Mainz, Germany

Biomaterials such as bone or nacre exhibit remarkable material properties which originate from the combination of hard and soft materials, interactions at organic/inorganic interfaces, and hierarchical organization that involves structure formation from the nanoscale to mesoscopic levels. Multiscale simulations combining models on several levels of resolution are being developed to approach such systems on a wide range of relevant length and timescales. Such an approach aims at obtaining both a (microscopic) understanding of the relevant interactions in these systems as well as the possibility to study the structure formation and aggregation processes involved. This requires systematic development of reduced resolution models, including an understanding of their thermodynamic and structural properties. An important issue is the question of transferability of reduced resolution models to different environments and their ability to reproduce conformational transitions, for example at an interface or upon interactions with a mineral surface.

The conditional reversible work method for systematic coarse graining of complex fluids

Nico F. A. van der Vegt

Technical University Darmstadt, Center of Smart Interfaces, Darmstadt, Germany

Systematically coarse grained models for complex fluids usually lack chemical and thermodynamic transferability. In my talk, I will discuss our ongoing work on developing nonbonded interaction potentials for coarse grained simulations of molecular liquids and polymers. Our recently developed conditional reversible work (CRW) method will be discussed and the thermodynamic transferability of the resulting potentials will be compared with results obtained with alternative coarse graining methods. The examples discussed in my work include 3-site models of hexane and toluene as well as coarse grained models of amorphous polymers and polyelectrolytes in solution. Finally, I will show a few applications of the developed models, including hierarchical simulations of glassy polymer surfaces, polymer crystallization and modeling of polymer permeabilities.

Simulation of soft coarse-grained models for membranes

Marcus Mueller, Kostas Daoulas, Marc Fuhrmans, Martin Hoemberg, Giovanni Marelli

Goerg-August University, Institute for Theoretical Physics, Goettingen, Germany

We investigate the static and dynamic properties of a coarse-grained solvent-free model for lipid membranes where the non-bonded interactions are inspired by a weighted-density functional. Within the mean-field approximation, the model parameters can be related to basic physical properties of the membrane like the density and compressibility of the hydrophobic core. The phase behavior of the model is studied and methods to calculate free-energies are illustrated. The ability of the coarse-grained model to capture the collective membrane dynamics (viscosity, inter-monolayer friction, dynamics of bilayer undulations) is discussed.

Multiscale modeling and simulation of liquids and liquid-solid interfaces

Luigi Delle Site

Free University of Berlin, Institute for Mathematics, Berlin, Germany

I will present multiple scale strategies to study macroscopic properties of liquids and liquid-solid interfaces via Simulation. The aim is to bridge the specific chemistry of single molecules to the macroscopic properties produced by a large number of them. In this context, I will discuss, in particular, the adaptive resolution coupling of scales and its extension to quantum systems.

Mechanics of biomaterials: How proteins propagate forces

Frauke Graeter

Heidelberg Institute for Theoretical Studies, Molecular Biomechanics, Heidelberg, Germany

The mechanics of complex structures like proteins is determined by the way force distributes through the structure.

How can the force-bearing elements of a structure be detected? We recently developed a technique termed Force Distribution Analysis (FDA), based on standard Molecular Dynamics simulations, to reveal the propagation of stress through a molecular structure. FDA is the atomistic-scale analogue of Finite Element Analysis for macroscopic structures.

I will describe the concept of FDA, its ability to bridge different length scales, and recent applications to different protein systems with mechanical function. Most importantly, our results for silk fiber mechanics and synthetic fiber design will be discussed.

Tuning the mechanical properties of proteins: From single molecule to biomaterials

Hongbin Li

University of British Columbia, Department of Chemistry, Vancouver, Canada

Elastomeric proteins underlie the elasticity of natural adhesives, cell adhesion and muscle proteins. Single molecule force spectroscopy has made it possible to directly probe the mechanical properties of elastomeric proteins at the single molecule level. Combining single molecule atomic force microscopy (AFM) and protein engineering techniques, researchers have started to understand the molecular design principles of elastomeric proteins and use such knowledge to engineer novel elastomeric proteins of tailored nanomechanical properties. Here I describe how we use single molecule AFM studies to guide the design of artificial elastomeric proteins to mimic the mechanical properties of the giant muscle protein titin, and employ such proteins to engineer biomaterials that mimic the passive elastic properties of muscles. The passive elasticity of muscle is largely governed by the I-band part of titin, a complex molecular spring composed of a series of individually folded immunoglobulin-like (Ig) domains as well as largely unstructured unique sequences. These mechanical elements have distinct mechanical properties, and when combined, they provide desired passive elastic properties of muscle, which are a unique combination of strength, extensibility and resilience. Our prior single molecule AFM studies demonstrated that the macroscopic behavior of titin in intact myofibrils can be reconstituted by combining mechanical properties of these mechanical elements measured at the single-molecule level. Based on such insight, we used well-characterized protein domains GB1 and resilin to engineer artificial elastomeric proteins that mimic the molecular architecture of titin. We showed that these artificial elastomeric proteins can be photocrosslinked and cast into solid biomaterials. These biomaterials behave as rubber-like materials showing high resilience at low strain and as shock absorber-like materials at high strain by effectively dissipating energy. These properties are comparable to passive elastic properties of muscles within the physiological range of sarcomere length and thus these materials represent a novel muscle-mimetic biomaterial. The mechanical properties of these biomaterials can be fine-tuned by adjusting the composition of the elastomeric proteins, providing possibilities for molecular level engineering of macroscopic mechanical properties of biomaterials. We anticipate that these novel biomaterials will find applications in tissue engineering as scaffold and matrix for artificial muscles.

Simulation approaches to friction in proteins and polymers

Roland Netz

Technical University Munich, Department of Physics, 14195 Berlin, Germany

The dynamic properties of polymers and proteins are governed not only by friction with the solvent but also by internal friction effects.
Insight can be gained from all-atomistic simulations of short peptides with explicit water that reach the experimentally relevant and time scales.

Two connected lines of work will be discussed:

1) On surfaces, the friction coefficient of bound polymers is very low on hydrophobic substrates, which is traced back to the presence of a vacuum layer between substrate and water, which forms a lubricating cushion on which a polymer can glide [1]. Conversely, friction forces on hydrophilic substrates are large. A modified Amonton´s law is introduced, which generally describes the dynamics of hydrogen-bonded matter on the nano-scale [2].

2) The contribution of internal friction to the folding of peptides is traditionally probed by changing the solvent viscosity and extrapolating down to vanishing solvent viscosity. We apply the same procedure to simulations of short disordered and alpha-helix forming peptides, the results can be favorably compared with results borrowed from polymer theory.

References

[1] Polypeptide friction and adhesion on hydrophobic and hydrophilic surfaces: A molecular dynamics case study A. Serr, D. Horinek and R.R. Netz, JACS 130, 12408 (2008).
[2] A. Erbas, D. Horinek, R.R. Netz, to be published.
[3] J. Schulz, L. Schmidt, J. Dzubiella, R.R. Netz, to be published.

Multi-scale modeling of DNA derivatives

Daniele Varsano and R. Di Felice

1) University of Rome La Sapienza, Department of Physics
2) Centro S3, CNR Istituto di Nanoscienze

DNA molecules have always retained a special place in scientific investigation, for biological/medical issues. Lately, DNA is also attracting interest for several potential applications in the field of nanotechnology, due to its stability (in solution), to its one-dimensional character, and to the regular π-stacking, along with the unique properties of self-assembling and recognition.

In order to calculate electronic, optical and hole-transport properties of these molecules, the effect of intrinsic structural movements cannot be neglected and multi-scale scale techniques can be adopted.

In this talk I will first show how the optical activity of organic molecules may dramatically depend on the dynamical modifications of the molecular configuration induced by thermal fluctuations, by combining Car-Parrinello molecular dynamics and linear-response TDDFT calculations. The results of this combined approach indicate that no static model can properly describe these effects, not even if the dielectric screening of the solvent is implicitly accounted for by a polarizable continuum model. For DNA molecules of interest, Car-Parrinello simulations are still too computationally cumbersome.

Alternatively, the dynamics can be accounted for by classical molecular dynamics. Representative structures are then extracted from the trajectory, pruned to relevant sites and used for quantum electronic structure calculations for the ground state and excited states.

We have applied this multi-scale protocol to various DNA motifs, including triplexes, quadruplexes and modified dsDNA, and I will illustrate examples of the influence of thermal fluctuations on the optical spectra computed for small fragments at the TDDFT level.

Charge migration and heat phenomena in biomolecular systems: Two sides of the same medal?

Gianaurelio Cuniberti

Dresden University of Technology, Institute for Materials Science, 01062 Dresden, Germany

Charge migration is a ubiquitous phenomenon with profound implications throughout many areas of chemistry, physics, biology and materials science. The long-term vision of designing functional materials with pre-defined molecular scale properties has triggered an increasing quest to identify prototypical systems where truly inter-molecular conduction pathways play a fundamental role. Such pathways can be formed due to molecular organization of various organic materials and are widely used to discuss electronic properties at the nanometer scale. Molecular systems on the other hand could also efficiently provide strategies for phonon transport which results in the possibility of tailoring its thermal transport properties. In this talk, I will illustrate how recent important contributions to unimolecular electronics research can help -on a similar footing- in describing heat conductance and the possible consequences for exploiting such effects.

References

[1] M. H. Rümmeli et al., Advanced Materials, to appear (2011).
[2] E. Diaz et al., Physical Review B, to appear (2011); arXiv:1103.3443.
[3] V. Bezugly et al., ACS Nano 5, 4997 (2011).
[4] J. Haskins et al., ACS Nano 5, 3779 (2011).
[5] H. Kleemann, et al., Nano Letters 10, 4929 (2010).
[6] M. W. Shinwari et al., Advanced Functional Materials 20, 1865 (2010).
[7] R. Gutierrez et al., Physical Review Letters 102, 208102 (2009).
[8] D. Dulic et al., Angewandte Chemie Intnl Edition 48, 8152(2009).

Modeling transport of biomolecules through synthetic nanochannels

Aleksei Aksimentiev

University of Illinois at Urbana-Champaign, Department of Physics, Urbana, US

Nanopores and nanochannels are convenient systems for detection and manipulation of single biomolecules as their geometry offers, in principle, the means to control both the conformation of biomolecules and the force the biomolecules are subjected to. In practice, however, neither the force nor the conformations of biomolecules are known, as the systems are too small to be imaged using conventional experimental approaches. In recent years, computer modeling and, in particular, molecular dynamics simulations have emerged as an alterative imaging method that can provide not only atomically precise descriptions of microscopic processes inside nanopores and nanochannels but also directly relate such processes to experimentally measurable observables. This talk will summarize recent advances in modeling nanoscale transport systems, in particular our recent attempts to control the force on DNA in a nanochannel, detect the sequence of a DNA molecule by measuring the nanopore ionic current, and model transport of small solutes through nanofluidic systems that have sticky surfaces.

A coarse grained QM/MM approach for the description of hole transfer in DNA

Marcus Elstner

Karlsruhe Institute of Technology, Department of Physical Chemistry, Karlsruhe, Germany

Charge transfer in DANN has received much attention in the last years due to ist role in oxidative damage an repair in DANN, but also due to possible applications of DANN in nano-electronics. Despite intense experimental an theoretical efforts, the mechanism underlying long range hole transport is still unresolved. This is in particular due to the fact, that charge transfer sensitively depends on the complex structure an dynamics of DANN an the interaction with the solvent environment, which could not be addressed adequately in the modeling approaches up to now. We present a new computational strategy to evaluate the charge-transfer (CT) parameters for hole transfer in DANN. Based on a fragment orbital approach, site energies an coupling integrals for a coarse grained tight binding description of the electronic structure of DANN can be rapidly calculated using the approximate Density Functional method SCC-DFTB. Environmental effects are captured using a combined quantum mechanics/molecular mechanics (QM/MM) coupling scheme an dynamical effects are included by evaluating these CT parameters along extensive classical molecular dynamics (MD) simulations. This methodology allows to analyze in detail several factors responsible for CT in DANN. The fluctuations of the counterions, strongly counterbalanced by the surrounding water, leads to large fluctuations of the site energies, which govern the hole propagation along the DANN strand, while the electronic couplings depend strongly on DANN conformation an are not affected by the solvent. Using this methodology, the time course of the hole can be followed by propagating the hole wave function using the time dependent Schrödinger equation for the coarse grained Hamiltonian.

Abstracts of Posters

Adhesion of proteins on glass surfaces: Towards a QM/MM approach

P01

Anke Butenuth, Gianpietro Moras

University of Freiburg, Fraunhofer Institute for Mechanics of Materials IWM, Freiburg, Germany

Hybrid methods (which combine both the accuracy of density functional theory (DFT) to describe chemical processes and the ability of classical force fields to deal with larger systems) represent an interesting approach to study the bio/material interface. However, in silica systems, it is not clear how to choose the size of the quantum-mechanical region as to sufficiently reproduce accurate forces. Thus, we have studied silica clusters from several silica systems with different embedding schemes to gain information on the convergence of the quantum-mechanical forces with cluster size.

Another aspect that needs further development in order to proceed with the development of accurate QM/MM approaches is the classical description of the interaction between a solution and deprotonated sites on silica surfaces. As it is known that the amorphous silica surface in ambient water is negatively charged, suitable parametrization of classical force fields are needed. Here, we use DFT to calculate the charge distribution for such systems within two different charge concepts (Bader/ESP) and we discuss the implications from our results for the parametrization of classical potentials for these systems.

Protein-ligand binding free energies from large-scale DFT calculations with the ONETEP program

P02

Stephen Fox (1), Thomas Fox (2), Christofer S. Tautermann (2), Chris-Kriton Skylaris (1)

(1) School of Chemistry, University of Southampton, Southampton, SO17 1BJ, UK; (2) Boehringer Ingelheim Pharma GmbH & Co. KG, Lead Identification and optimization Support, 88397 Biberach, Germany

The calculation of free energy of binding for small molecules to proteins is a very important problem in drug optimisation and many approaches for such calculations have been developed [1].
The Molecular Mechanics Poisson-Boltzmann Surface Area (MM-PBSA) is one such method, in which the free energy of binding is obtained as a sum of the differences in energies of the complex, receptor and ligand (ΔH), and the differences in solvation energies (ΔGsolv), averaged over a structural ensemble taken from a Molecular Dynamics simulation. Conventional methods use classical force fields to calculate the energies and the PBSA implicit solvent model for the solvation energy. This can be a serious limitation to the accuracy of this method due to the empirical nature of the force field used to describe the system, and the neglect of electrons in force fields which leads to the inability to properly describe polarisation or to account for electron transfer.
In this work, the energies are calculated using Density Functional Theory (DFT) on the entire protein-ligand system and the solvation energy with a new minimum parameter implicit solvent approach with the self-consistent QM calculation [2], all within the ONETEP program [3]. We present application of this QM-PBSA [4] method to a number of small aromatic ligands bound in the polar cavity of the T4-lysozyme mutant L99A-M102Q [5].

References

[1] B. O. Brandsdal, F. Osterberg, M. Almlof, I. Feierberg, V. B. Luzhkov and J. Aqvist, Advances in Protein Chemistry, 66, 123-156 (2003).
[2] J. Dziedzic, H. H. Helal, C.-K. Skylaris, A. A. Mostofi and M. C. Payne, Accepted to EPL.
[3] C.-K. Skylaris, P. D. Haynes, A. A. Mostofi and M. C. Payne, J. Chem. Phys. 122, 084119 (2005).
[4] D. J. Cole, C.-K. Skylaris, E. Rajendra, A. R. Venkitaraman and M. C. Payne. Europhysics Letters 91, 37004 (2010); S. Fox, H. Wallnoefer, T. Fox, C. Tautermann, and C.-K. Skylaris. J. Chem. Theor. Comput. 7, 1102 (2011).
[5] B. Q. Wei, W. A. Baase, L. H. Weaver, B. W. Matthews, and B. K. Shoichet, J. Mol. Biol. 322, 339 (2002).

Simulation of peptide - ion interactions during the early stages of biomineralisation

P03

Jens Kahlen, Christine Peter, Davide Donadio

Max Planck Institute for Polymer Research, Mainz, Germany

The crystallisation of inorganic compounds such as calcium oxalate, zinc oxide or calcium carbonate is of great academic and industrial relevance. Biomacromolecules such as proteins can have a tremendous influence on the kinetics of crystal growth and resulting morphologies of the crystals formed in solution. This complex process is governed by many physical and chemical phenomena that occur on different time and length scales. Understanding these phenomena and their interplay would provide a great contribution towards the design of new materials.
Atomistic simulations can be a valuable tool to analyse the dependence of resulting material properties of these crystals from processes on a molecular scale. Our current research activities are concerned with molecular modeling of the crystallisation of calcium-containing minerals in the presence of peptides such as oligoglutamates. The early stages of this biomineralisation process are controlled by interactions of single ions and peptide molecules in solution. Therefore, we perform classical atomistic Molecular Dynamics calculations to analyse the mutual influence of the adhesion of calcium ions to oligoglutamates and the conformations of the peptides. With the information obtained through these studies it will then be possible to investigate the adhesion of peptides to the crystal surface which presumably alters crystal growth. In order to validate the applied methods and forcefields through comparison between simulation results and experimental data, cooperation with experimentalists has been initiated.

From atomistic modeling to exciton dynamics and two-dimensional spectra of light-harvesting complexes

P04

Carsten Olbrich (1), Thomas la Cour Jansen (2), Jörg Liebers (1),
Mortaza Aghtar (1), Johan Strümpfer (3), Klaus Schulten (3),
Jasper Knoester (2), and Ulrich Kleinekathöfer (1)

(1) Jacobs University Bremen, Campusring 1, 28759 Bremen, Germany
(2) University of Groningen, Zernike Institute for Advanced Materials, Nijenborgh 4, 9747 AG Groningen, The Netherlands
(3) University of Illinois at Urbana-Champaign, Center for Biophysics and Computational Biology and Beckman Institute, Urbana, Illinois, USA

The experimental observation of long quantum coherences in the Fenna-Matthews-Olson (FMO) light-harvesting complex has steered considerable effort to explain these findings. Based on molecular dynamics simulations, electronic structure calculations for the vertical excitation energies of the individual bacteriochlorophylls along the trajectory have been performed for the green sulphur bacterium Chlorobaculum tepidum. In addition, the electronic couplings between the pigments have been determined in a time-dependent manner as well. The distribution of energies and couplings are analyzed together with possible spatial correlations. In a subsequent step, averaged wave packet dynamics are used to determine the exciton dynamics in the system. Finally, the time-dependent Hamiltonian is used to determine linear and two-dimensional spectra. This allows a direct comparison with experiment. In summary, atomistic simulations have been employed to directly determine spectroscopic properties of the FMO complex at ambient temperatures.

Specific binding peptides on titania surfaces **P05**

Wenke Friedrichs (1), Susan Köppen (2), Walter Langel (1)

(1) Institute for Biochemistry, Biophysical Chemistry, University of Greifswald, Germany
(2) University of Bremen, Hybrid Materials Interfaces, Faculty of Production Engineering and Bremen Center for Computational Materials Science, Bremen, Germany

“Genetically engineered peptides for inorganics” (GEPI) [1] are short sequences of about 10 amino acids acting as optimized binders on specific inorganic materials. Even though good binders on one specific material have been found to have very similar sequences, also the secondary structure of those peptides strongly influence the binding to materials surfaces [1]. Those specific binders are of major interest for technical applications while possibly using them for specific biofunctionalization of materials surfaces without the complex handling of whole protein structures.
The observed significant dependence of the adsorption properties on the sequences was not well understood so far. Therefore, results of the investigation of the adsorption of two different peptide sequences on titania surfaces by means of classical molecular dynamics simulations will be presented here. The sequences are chosen to be known as examples for good and bad binders on standard TiO2 surfaces, respectively, in the experiment [2].
First analysis of the secondary structure resulted in a similar ratio of turn as well as helix regions, even though, the distribution of amino acids working as helix builders is quite different. During first simulations of single peptide adsorption on rutile surfaces with varied initial configurations, the experimental observation of the classification into “good” and “bad” binders could be completely reproduced. Competitive adsorption of up to three molecules in one simulation cell showed clustering of both sequences. Whereas, for the good binding sequences the adsorption sides are not occupied by the intermolecular interaction resulting in adsorption of a peptide film, the weak adsorption of a single bad binder could not be reproduced with more than one molecule in the simulation cell. Here, clustering of the peptides without surface adsorption have been observed.

References

[1] Tamerler et al, Peptide Science 94 (2010) 78-94.
[2] priv. communication, M. Sarikaya.

Non-adiabatic simulation of charge transfer in biomolecules **P06**

Tomas Kubar, Ben Woiczikowski and Marcus Elstner

Karlsruhe Institute of Technology, Institute of Physical Chemistry, Karlsruhe, Germany

Coarse-grained multi-scale method based on DFT for the simulation of charge transfer in biomolecular systems is presented. The fragment-orbital ansatz and the use of approximative DFT method SCC-DFTB to compute the charge-transfer parameters allow to simulate the dynamics of excess charge on a nanosecond time scale, not having to neglect the important effects of structural fluctuations and solvent. Non-adiabatic schemes to propagate the wave function of the excess charge have been implemented: simultaneous integration of coupled equations of motion for QM and MM within the framework of time-dependent DFT, as well as diabatic surface hopping approach. In the case of hole transfer in solvated DNA, polarization of solvent is the dominant factor affecting the transfer. The features of the process as described with the various simulation schemes are discussed.

Development of an implicit solvent coarse-grained model for electrolytes in contact with mineral surfaces

P07

Jia-Wei Shen (1), Chunli Li (2), Nico F. A. van der Vegt (2), Christine Peter (1)

(1) Max Planck Institute for Polymer Research, Ackermannweg 10, 55128 Mainz, Germany
(2) Technical University of Darmstadt, Center of Smart Interfaces, Petersenstrasse 32, 64287 Darmstadt, Germany.

Formations of many biological materials such as bone or nacre are processes and mechanisms on many hierarchical levels – from mesoscopic properties of the materials down to microscopic (atomistically detailed) interactions. To understand the basic principles of hierarchical structures of these biological materials, we aim at developing multiscale simulation approachs to study the formations and properties of natural and synthetic mineral/organic nanocomposites such that we can systematically link models on several hierarchical levels. As in the biomineralization and synthetic mineral/organic nanocomposites, the electrostatic interactions play a significant role in these complex systems, we start the development of multiscale simulation methodology from an implicit solvent Coarse-Grained model for electrolyte in the solution. By using a concentration-dependent dielectric permittivity, we found that the Coarse-Grained model parameterized based on ion-ion association at infinite dilution (i.e. based on pair potentials of mean force in explicit water simulations) can well reproduce the structure and thermodynamics properties of electrolyte solution at the atomistic level and can be made transferable to wide range of electrolyte concentrations. By further “thermodynamics property-based” and “structure-based” correction, the Coarse-Grained model could even extend to very high electrolyte concentration (close to saturated concentration). On the basis of the above methodology, we further extended the coarse-grained model to the system of electrolyte in contact with mineral surfaces, where effective ions-surface interactions are obtained from potentials of mean force calculations and the solvent effect in inhomogeneous system has been taken into consideration.

Soft matter from an atomic-scale condensed matter starting point **P08**

Elisa Londero, Elsebeth Schröder, Per Hyldgaard

Chalmers University of Technology, Microtechnology and Nanoscience Department, Goeteborg, Sweden

Full quantum physical calculations of biomolecular forces hold promise for predicting structure and function without input and in the presence of charge transfer. Being non-empirical, they deliver an atomic scale characterization of binding and relaxations, for example at material interfaces where few other detailed probes are available. Until recently however, our best condensed matter tool for non-empirical description, Density Functional Theory (DFT) was not capable of addressing soft matter and biomolecular problems. The issue is not only a huge number of atoms but also a failure of traditional approximations for the density functional.
The DFT functional vdW-DF [1] has proven to be a strong candidate for a new predicting condensed matter description [2]. It includes an account of dispersive interactions by introducing a true nonlocality in the density functional. We show that our functional has the potential to describe extended systems with the accuracy of DFT, thus opening the way to the description of complex soft phenomena, such as adsorption/adhesion, catalytic reactions or nanoscale lubrication.

References

[1] M. Dion et al., Phys. Rev. Lett. 92, 246401 (2004); T. Thonhauser et al., Phys. Rev. B 76, 125112 (2007).
[2] D. C. Langreth et al., J. of Physics: Cond. Matt. 21, 084203 (2009).

Probing the transport of ionic liquids in aqueous solution through nanopores

P09

Niraj Modi, Pratik Raj Singh, Kozhinjampara R. Mahendran, Robert Schulz, Mathias Winterhalter, Ulrich Kleinekathoefer

School of Engineering and Science, Jacobs University Bremen, Campus Ring 1, 28759 Bremen, Germany

The temperature-dependent transport of the ionic liquid 1-butyl-3-methyl imidazolium chloride (BMIM-Cl) in aqueous solution is studied theoretically and experimentally. Using molecular dynamics simulations and ion-conductance measurements, the transport is examined in bulk as well as through a biological nanopore, i.e., OmpF and its mutant D113A. This investigation is motivated by the observation that aqueous solutions of BMIM-Cl drastically increase the average residence time of DNA or antibiotics through nanopores in electrophysiological measurements. This makes BMIM-Cl an interesting alternative salt to improve the time resolution. In line with previous investigations of simple salts, the size of the ions and their orientation adds another important degree of freedom to the ion transport, thereby slowing down the transport through nanopores. An excellent agreement between theory and conductance measurements is obtained for wild-type OmpF and a reasonable agreement for the mutant. Moreover, all-atom simulations allow an atomistic analysis revealing molecular details of the rate-limiting ion interactions with the channel.

Voltage-controlled switchable surfaces using polyelectrolyte brushes

P10

F. Rodriguez-Ropero N. F. A. van der Vegt

Technical University of Darmstadt, Computational Physical Chemistry, Center of Smart Interfaces, Petersenstrasse 32, 64287 Darmstadt, Germany

Polymer brushes are a specific kind of macromolecule formed by polymer chains grafted by an end group to a solid surface in a number high enough so that the chains are stretched away from the interface due to steric hindrance or electrostatic repulsion between neighboring polymer units. It is precisely this deformed configuration at equilibrium what differentiates polymer brushes from their unperturbed counterparts conferring them a unique set of properties. The distinctive architecture of polymer brushes and the possibility of easily tuning their surface by adding different functional groups make them a flexible tool to modify the surface properties of materials and modulate their sensitivity towards specific stimuli without affecting the bulk properties.

In this work we use Molecular Dynamic simulations to examine the extension/collapse transition of a diblock copolymer brush composed of N,N'-Dimethylacrylamide (DMAA) and Methacrylic acid (MAA) in response to an external electric field perpendicular to the grafting surface considering different grafting densities and salt concentrations.

Water adsorption on (1-210): Electronic and dynamic properties **P11**

Svea Sauer (1), Susan Köppen (2), Lucio Colombi Ciacchi (2),
Thomas Frauenheim (1)

(1) University of Bremen, BCCMS, CMS, Am Fallturm 1, 28359 Bremen, Germany;
(2) University of Bremen, BCCMS, HMI, Am Fallturm 1, 28359 Bremen, Germany

Owing to the prevalent role of zinc oxide in processing reactions involving water, the zinc oxide water interface is an ongoing field of research. In our study we focus on the (1-210) surface of zinc oxide. Thereby we investigate the adsorption starting from a single water molecule up o a full monolayer. Calculations are performed using ab initio DFT, a reactive forcefield and the DFTB+ code. Apart from static calculations, molecular dynamics simulations are used to analyze the influence of bulk water on the adsorption configurations.

Development of an implicit solvent coarse-grained model for electrolytes in contact with mineral surfaces

P12

Jia-Wei Shen (1), Chunli Li (2), Nico F.A. van der Vegt (2), Christine Peter (1),

(1) Max Planck Institute for Polymer Research, Ackermannweg 10, 55128 Mainz, Germany
(2) Technical University of Darmstadt, Center of Smart Interfaces, Petersenstrasse 32, 64287 Darmstadt, Germany

Formations of many biological materials such as bone or nacre are processes and mechanisms on many hierarchical levels – from mesoscopic properties of the materials down to microscopic (atomistically detailed) interactions. To understand the basic principles of hierarchical structures of these biological materials, we aim at developing multiscale simulation approachs to study the formations and properties of natural and synthetic mineral/organic nanocomposites such that we can systematically link models on several hierarchical levels. As in the biomineralization and synthetic mineral/organic nanocomposites, the electrostatic interactions play a significant role in these complex systems, we start the development of multiscale simulation methodology from an implicit solvent Coarse-Grained model for electrolyte in the solution. By using a concentration-dependent dielectric permittivity, we found that the Coarse-Grained model parameterized based on ion-ion association at infinite dilution (i.e. based on pair potentials of mean force in explicit water simulations) can well reproduce the structure and thermodynamics properties of electrolyte solution at the atomistic level and can be made transferable to wide range of electrolyte concentrations. By further “thermodynamics property-based” and “structure-based” correction, the Coarse-Grained model could even extend to very high electrolyte concentration (close to saturated concentration). On the basis of the above methodology, we further extended the coarse-grained model to the system of electrolyte in contact with mineral surfaces, where effective ions-surface interactions are obtained from potentials of mean force calculations and the solvent effect in inhomogeneous system has been taken into consideration.

Collision dynamic of nanodroplet embedded macromolecules **P13**

Si Neng Sun, Herbert M. Urbassek

Technical University Kaiserslautern, Department of Physics

Theoretical understanding of the response of macromolecules to collision processes is important for many aspects, for example the Impact Desolvation of Electrosprayed Microdroplets (IDEM), which has the purpose to isolate a single Bio- (or Macro-) molecule from their solution without to damage them. The dynamic of analyte molecule involves energy distibution/coupling in the internal degrees of freedom (vibrational modes) and overcoming of transition states, we present a method to analyse energy distribution and transition states in model systems using covariance analysis in the framework of molecular dynamics.

This method maps the complex potential landscape in each reaction coordinate to an effective harmonic potential, crossing of a transition state can be identified by the change of vibration frequencies; and also the energy distribution can be easily obtained in this effective harmonic system. In the ground state, this method approaches to the normal mode analysis, while in finite temperatures, the anharmonic vibrations are maped. The molecular trajectories can be projected on the covariance modes, to analyse the dynamic of molecule and get instantaneous energy distributions.

Using this method, collision process of nanodroplet embedded polymers are studied. After the collisions, polymers are stretched due to shock compression but they resume their dimension after 100 ps. We find, that the first mode is responsible for the mechanical stretch, and the equilibrium in internal degrees of freedom has close relationship to the resuming of the molecule form.

Conformational features of arenicin – from the bulk to the air-water interface and through a model cell membrane

P14

Maria Velinova (1,2), N. Ilkova (1), A. Ivanova (1), A. Tadjer (1), S. J. Marrink (2)

(1) University of Sofia, Faculty of Chemistry, 1 James Bourchier Ave., 1164 Sofia, Bulgaria;
(2) University of Groningen, Groningen Biomolecular Science and Biotechnology Institute, Groningen, The Netherlands

Antimicrobial peptides (AMPs) are short amphipathic cationic trans-membrane proteins extracted from various lower organisms. A wide range of antimicrobial activity is measured for AMPs, the latter playing a key role for the protection and enhancement of the native immune system of the higher organisms. AMPs attract the attention of medical scientists as they are an appealing alternative to overcoming the problem with bacterial resistivity to antibiotics. Nevertheless, the exact mechanism of selective attachment to the membrane of the target cell and ist subsequent necrosis are still not fully elucidated and are shown to be peptide-dependent. The novel arenicins found recently in the coelomocytes of marine polychaeta lugworm Arenicola marina are an interesting research target in this respect.
For determination of the conformation of arenicin in aqueous solution and at the air/water interface all-atom molecular dynamics (MD) simulations (NPT/298 K) with the AMBER03 force field in explicit water (TIP3P) with PBC applied were carried out. Arenicin retained ist b-hairpin structure during simulations, although the residues close to strand ends were found to escape from the ideal hairpin conformation. The structures resulting from the computer simulation were found in fairly good agreement with experimental data [1]. For clarification of the mechanism of interaction of arenicin with membrane lipids, coarse-grained MD simulations (NPT/323 K) with the MARTINI force field were performed. Analyses of the results for the selected systems allow establishment of the pore properties at a multi-scale level and the study of the poration mechanism of the arenicin peptides.

References

[1] Travkova, O. G.; Andrä, J.; Mohwald, H.; Brezesinski G. ChemPhysChem 2010, 11, 3262.

Extracting protein dynamics from single-molecule experiments using dynamic deconvolution

P15

Yann von Hansen (1), Michael Hinczewski (1,2), Roland R. Netz (1,3)

1) Technical University of Munich, Physics Department
2) University of Maryland, Institute for Physical Science and Technology
3) Free University Berlin, Physics Department

The concept of a protein diffusing in its free-energy folding landscape has been fruitful for both theory and experiment. Extensive all-atom simulations of small proteins and peptides in implicit and explicit solvent [1-3] have recently shown pronounced variations of the diffusivity – a measure of the internal friction arising from the transient breaking and reformation of bonds in the protein structure – along the reaction coordinate. Moreover, the analysis of the peptide kinetics in salt-solutions revealed that salt not only specifically modifies equilibrium properties (free-energy landscapes), but can also induce kinetic barriers due to individual ion binding, which are reflected in changes of the state-dependent diffusivity [3].

Time-resolved single-molecule biophysical experiments yield data that contain a wealth of dynamic information, in addition to the equilibrium distributions derived from histograms of the time series. In typical force spectroscopic setups the molecule is connected via linkers to a readout device, forming a mechanically coupled dynamic network. Deconvolution of equilibrium distributions, filtering out the influence of the linkers, is a straightforward and common practice [4-6]. We have developed an analogous dynamic deconvolution theory [7] for the more challenging task of extracting kinetic properties of individual components in networks of arbitrary complexity and topology. Our method determines the intrinsic linear response functions of a given object in the network, describing the power spectrum of conformational fluctuations. The practicality of our approach is demonstrated for the particular case of a protein linked via DNA handles to two optically trapped beads using Brownian dynamics simulations. Each well in the protein free energy landscape (corresponding to folded, unfolded, or possibly intermediate states) will have its own characteristic equilibrium fluctuations. The associated linear response function is rich in physical content, because it depends both on the shape of the well and its diffusivity.

References

[1] G. Hummer, R. Best, Proc. Natl. Acad. Sci. USA 107, 1088 (2010).
[2] M. Hinczewski, Y. von Hansen, J. Dzubiella, R.R. Netz, J. Chem. Phys. 132, 245103 (2010).
[3] Y. von Hansen, I. Kalcher, J. Dzubiella, J. Phys. Chem. B 114, 13815 (2010)
[4] M.T. Woodside et al., Science 314, 1001 (2006).
[5] M.T. Woodside et al., Proc. Natl. Acad. Sci. USA 103, 6190 (2006).
[6] J.C.M. Gebhardt, T. Bornschlögl, M. Rief, Proc. Natl. Acad. Sci. USA 107, 2013 (2010).
[7] M. Hinczewski, Y. von Hansen, R.R. Netz, Proc. Natl. Acad. Sci. USA 107, 21493 (2010).

Bottom-up multiscale simulations of silk fiber mechanics **P16**

Senbo Xiao, Murat Cetinkaya, Frauke Graeter

Heidelberg Institute for Theoretical Studies, Molecular Biomechanics, Heidelberg, Germany

Silk is an intriguing protein-based material that combines elasticity and strength to an extent not yet reached by any synthetic material today. Silk fibers are composed of highly-ordered beta-sheet crystals and an amorphous peptide matrix that both contribute to the outstanding mechanical properties. However, how the way of organization of these two components affects silk fiber mechanics has remained unclear. Here, we combine large scale molecular dynamics simulations, a novel atomistic force distribution analysis, and finite element methods to quantify the mechanics of silk fibers and its components in a bottom-up approach. Namely, elastic and rupture parameters of silk composite units as extracted from all-atom molecular simulations serve as element properties in finite element analysis [1,2]. By doing so, we can derive macroscopic fiber mechanics from the nano-structure, in quantitative agreement with experimental results. One of our most striking predictions is that a serial arrangement of silk crystalline units in the fiber, as commonly observed in form of lamellae for other block copolymers, outperforms a random distribution of crystals, in harp contrast to the current view of silk fiber organization [3]. We also show why the typical beta-strand length of eight residues in silk crystals is mechanically optimal [2]. Finally, a smaller cross-sectional area of silk crystals (~ 1nm2) in fibers provides a better reinforcement of the amorphous phase than larger ones. [4] We expect our straightforward multiscale approach to serve as a guideline for the design of silk-like synthetic materials.[5]

References

[1] S Xiao, W Stacklies, M Cetinkaya, B Markert, and F Gräter. Mechanical Response of silk crystalline units from force-distribution analysis. Biophys J, 2009.

[2] S Xiao, W Stacklies, C Debes, and F Gräter. Force distribution determines optimal length of β-sheet crystals for mechanical robustness. Soft Matter, 2010.

[3] M Cetinkaya, S Xiao, B Markert, W Stacklies, and F Gräter. Silk fiber mechanics from multiscale force distribution analysis. Biophys J, 2011.

[4] M Cetinkaya, S Xiao, F Gräter. Effects of crystalline subunit size on silk fiber. Soft Matter, 2011.

[5] M Cetinkaya, S Xiao, F Gräter. Bottom-up computational modeling of semi-crystalline fibers: from atomistic to continuum scale. Phys Chem Chem Phys, 2011.

Excess proton at water/hydrophobic interfaces: A Car-Parrinello MD study

P17

Chao Zhang, Emiliano Ippoliti, Yana Vereschchaga, Trung Hai Nguyen, Paolo Carloni

Computational Biophysics Lab German Research School for Simulation Sciences, 52425 Juelich, Germany RWTH Aachen University, 52056 Aachen, Germany Statistical and Biological Physics sector, SISSA, 34136 Trieste, Italy

Recently, both experimental and computational studies suggest that protons are preferably located on water/hydrophobic surfaces [1, 2]. The reasons are still unclear, although this is shown to be linked with the electronic structure of hydronium ions [3]. Therefore, a fully understanding of this phenomenon is highly desirable and will impact significantly on how we look at biological interfaces, such as presented in protein folding, protein/protein interaction and lipid membrane.

Thanks to a very large PRACE supercomputing grant (http://www.prace-project.eu/), we are able to investigate the structure and the energetics of an excess proton at the water/hydrophobic surface with ab initio molecular dynamics for a system size about 1800 atoms. The free energy profile of the proton to the surface, constructed by using the metadynamics method [4, 5], gives the state of the art answer to this fundamental question.

References

[1] P. Pohl Personal communication.
[2] S. Iuchi, H. Chen, F. Paesani, G. Voth J. Phys. Chem. B 2009, 113: 4017.
[3] K. N. Kudin and R. Car J. Am. Chem. Soc. 2008, 130: 3915.
[4] A. Laio and M. Parrinello Proc. Natl. Acad. Sci. USA 2002, 99: 12562.
[5] J. M. Park, A. Laio, M. Iannuzzi, M. Parrinello J. Am. Chem. Soc. 2006, 128: 11318.

List of Participants

Invited Speakers and Organisers

Dr. Barbara Aichmeyer
Max PIanck Institute of Colloids and Interfaces
Department of Biomaterials
Potsdam, Germany
aichmayer@mpikg.mpg.de

Prof. Dr. Gianaurelo Cuniberti
Dresden University of Technology
Institute for Materials Science
Dresden, Germany
office@nano.tu-dresden.de

Prof. Dr. Aleksei Aksimentiev
University of Illinois at Urbana-Champaign
Department of Physics
Urbana, US
aksiment@illinois.edu

Prof. Dr. Alessandro de Vita
King's College London
Physics Department
London, UK
Alessandro.de_vita@kcl.ac.uk

Dr. Markus Buehler
Massachusetts Institute of Technology
Department of Civil and Environmental
Engineering, Cambridge, US
mbuehler@MIT.EDU

Dr. Luigi Delle Site
Free University of Berlin
Institute of Mathematics
Berlin, Germany
dellsite@mpip-mainz.mpg.de

Prof. Dr. Helmut Coelfen
University of Konstanz
Department of Physical Chemistry
Konstany, Germany
Helmut.Coelfen@uni-konstanz.de

Prof. Dr. Marcus Elstner
University of Karlsruhe
Department of Physical Chemistry
Karlsruhe, Germany
marcus.elstner@kit.edu

Prof. Dr. Lucio Colombi Ciacchi
University of Bremen, BCCMS
Department of Production Engineering
Bremen, Germany
colombi@hmi.uni-bremen.de

Prof. Dr. Thomas Frauenheim
University of Bremen, BCCMS
Department of Physics
Bremen, Germany
frauenheim@bccms.uni-bremen.de

Dr. Stefano Corni
University of Modena
Center S3, Institute of Nanoscience
Modena, Italy
stefano.corni@nano.cnr.it

Dr. Colin Freeman
Sheffield University
Department of Materials Science and
Engineering, Sheffield, UK
c.l.freeman@shef.ac.uk

Dr. Gábor Csányi
Cambridge University
Engineering Laboratory
Cambridge, UK
gc121@cam.ac.uk

Dr. Frauke Graeter
Heidelberg Institute for Theoretical Studies
Department of Molecular Biomechanics
Heidelberg, Germany
frauke.graeter@h-its.org

Invited Speakers and Organisers

Prof. Dr. Hongbin Li
University of British Columbia
Department of Chemistry
Vancouver, Canada
hongbin@chem.ubc.ca

Prof. Dr. Kurosch Rezwan
University of Bremen
Advanced Ceramics
Bremen, Germany
krezwan@uni-bremen.de

Prof. Dr. Lutz Maedler
University of Bremen, Foundation Institute of Materials Science (IWT)
Bremen, Germany
maedler@iwt.uni-bremen.de

Prof. Dr. Mark Rodger
University of Warwick, Centrre for Scientific Computing, & Chemistry
Coventry, UK
p.m.rodger@warwick.ac.uk

Prof. Dr. Sievert-Jan Marrink
University of Groningen, Groningen Biomolecular Sciences and Biotechnology Institute (GBB),
Groningen, The Netherlands
s.j.marrink@rug.nl

Prof. Dr. Sandro Scandolo
The Abdus Salam International Centre for Theoretical Physics, Condensed Matter Group,
Trieste, Italy
scandolo@ictp.it

Prof. Dr. Elisa Molinari
University of Modena
Institute for Nanoscience
Modena, Italy
elisa.molinari@unimore.it

Prof. Dr. Klaus Schulten
University of Illinois at Urbana Champaign
Beckman Institute, Physics
Urbana, US
ddavis5@ks.uiuc.edu

Prof. Dr. Marcus Mueller
University of Goettingen
Institute for Theoretical Physics
Goettingen, Germany
mmueller@theorie.physik.uni-goettingen.de

Dr. Ralf Seidel
Dresden University of Technology
Biotechnology Center
Dresden, Germany
ralf.seidel@biotec.tu-dresden.de

Prof. Dr. Roland Netz
Technical University Munich
Department of Physics
Munich, Germany
netz@ph.tum.de

Dr. Chris-Kriton Skylaris
University of Southampton
Department of Chemistry
Southampton, UK
c.skylaris@soton.ac.uk

Dr. Christine Peter
Max Planck Institute for Polymer Research
Theory Group
Mainz, Germany
peter@mpip-mainz.mpg.de

Prof. Dr. Nico van der Vegt
Darmstadt University of Technology
Center of Smart Interfaces
Darmstadt, Germany
vandervegt@csi.tu-darmstadt.de

Invited Speakers and Organisers

Dr. Daniele Varsano
University of Rome "La Sapienza"
Department of Physics
Rome, Italy
daniele.varsano@roma1.infn.it

Dr. Tiffany Walsh
University of Warwick
Centre for Scientific Computing
Warwick, UK
walsh.tiffany@googlemail.com

Participants

Dr. Svetlana Baoukina
University of Calgary
Department of Biological Sciences
Calgary, Canada
s.baoukina@ucalgary.ca

Julian Bartels
University of Bremen, BCCMS
Department of Production Engineering
Bremen, Germany
julian.bartels@hmi.uni-bremen.de

Zhou Beifei
Heidelberg Institute for Theoretical Studies
Molecular Biomechanics
Heidelberg, Germany
z.beifei@gmail.com

Anke Butenuth
University of Freiburg
Fraunhofer Institute for Mechancis of Materials
Freiburg, Germany
but@iwm.fhg.de

Prof. Dr. Fabrizio Cleri
Université de Lille I
Institute of Nanotechnology
Villeneuve d'Ascq, France
fabrizio.cleri@univ-lille1.fr

Dr. Leonardo de Maria
Novozymes A/S
Protein Design
Bagsvaerd, Denmark
LeDM@novozymes.com

Tuan Do
University of Stuttgart
Institute of Technical Biochemistry
Stuttgart, Germany
datuan@itb.uni-stuttgart.de

Stephen Fox
University of Southampton
School of Chemistry
Southampton, UK
sjf2g08@soton.ac.uk

Wenke Friedrichs
University of Greifswald
Department of Biochemistry/ Biophysical Chemistry, Greifswald, Germany
wf041956@uni-greifswald.de

Meike Gummich
University of Bremen
Biophysics Institute
Bremen, Germany
mg@biophysik.uni-bremen.de

Jens Kahlen
Max Planck Institute for Polymer Research
Mainz, Germany
kahlen@mpip-mainz.mpg.de

Dr. James Kermode
King's College London
Department of Physics
London, UK
james.kermode@kcl.ac.uk

Dr. Susan Koeppen
University of Bremen, BCCMS
Department of Production Engineering
Bremen, German
koeppen@hmi.uni-bremen.de

Dr. Tomas Kubar
University of Karlsruhe
Karlsruhe Institute of Technology
Karlsruhe, Germany
tomas.kubar@kit.edu

Participants

Malte Launspach
University of Bremen
Biophysics Institute
Bremen, Germany
ml@biophysik.uni-bremen.de

Niraj Modi
Jacobs University Bremen
Computational Physics and Biophysics Group
Bremen, Germany
n.modi@jacobs-university.de

Dr. Chunli Li
Technical University of Darmstadt
Center of Smart Interfaces
Darmstadt, Germany
li@csi.tu-darmstadt.de

Letif Mones
University of Cambridge
Engineering Laboratory
Cambridge, UK
lam81@cam.ac.uk

Susanne Liese
Technical University Munich
Department of Physics
Munich, Germany
susanne.liese@mytum.de

Dr. Gianpietro Moras
University of Freiburg
Fraunhofer Institute for Mechanics of Materials
Freiburg, Germany
moras@iwm.fraunhofer.de

Elisa Londero
Chalmers University of Technology
Microtechnology and Nanoscience Department,
Göteborg, Sweden
londero@chalmers.se

Prof. Dr. Pablo Ordejon
Instituto de Ciencia de Materiales de Barcelona
CIN2
Barcelona, Spain
pablo.ordejon@cin2.es

Dr. Michael Maas
University of Bremen
Advanced Ceramics
Bremen, Germany
michael.maas@uni-bremen.de

Dr. Amedeo Palma
Italian National Research Council
I.S.M.N.
Monterotondo S. (RM), Italy
amedeo.palma@ismn.cnr.it

Dr. Faramarz Mehrnejad
Azerbaijan University of Tarbiat Moallem
Department of Cell and Molecular Biology
Tabriz, Iran
mehrnejad@azaruniv.edu

Dr. Lionel Perrin
INSA-Toulouse
Department of Physics
Toulouse, France
lionel.perrin@insa-toulouse.fr

Robert Meißner
University of Bremen
Fraunhofer IFAM
Bremen, Germany
robert.meissner@ifam.fraunhofer.de

Dr. Francisco Rodriguez-Ropero
Technical University of Darmstadt
Center of Smart Interfaces
Darmstadt, Germany
rodriguez@csi.tu-darmstadt.de

Participants

Andrzej Rzepiela
University of Freiburg
Physics Institute
freiburg, Germany
Andrzej.Rzepiela@physik.uni-freiburg.de

Si Neng Sun
Technichal University Kaiserslautern
Department of Physics
Kaiserslautern, Germany
sun@physik.uni-kl.de

Svea Sauer
University of Bremen, BCCMS
Department of Physics
Bremen, Germany
svea.sauer@bccms.uni-bremen.de

Maria Velinova
University of Sofia
Faculty of Chemistry
Sofia, Bulgaria
maria.velinova@chem.uni-sofia.bg

Lennart Schmidt
Technical University Munich
Department of Physics
Munich, Germany
lennart.schmidt@ph.tum.de

Yann von Hansen
Technical University Munich
Department of Physics
Munich, Germany
yann_von_hansen@ph.tum.de

Julian Schneider
University of Bremen, BCCMS
Department of Production Engineering
Bremen, Germany
schneider@hmi.uni-bremen.de

Senbo Xiao
Heidelberg Institute for Theoretical Studies
Molecular Biomechanics
Heidelberg, Germany
senbo.xiao@gmail.com

Dr. Jia-Wei Shen
Max Planck Institute for Polymer Research
Mainz, Germany
shenjw@mpip-mainz.mpg.de

Chao Zhang
RWTH Aachen University
Computational Biophysics Laboratory
Aachen, Germany
c.zhang@grs-sim.de

Xiao Shijun
Pattern Institute for Computational Biology
Shanghai, China
xiaoshijun@picb.ac.cn